Amendments to the Claims

Please cancel claims 13, 14 and 18-20 without prejudice. Please amend the remaining claims as shown below in the List of Claims.

List of Claims

1. (Currently amended) A process for the production of an L-amino acid product by fermentation comprising:
   a) culturing a recombinant microorganism from the Enterobacteriaceae family in a fermentation medium, wherein said recombinant microorganism produces said L-amino acid and wherein the yfiD ORF ~~and/or the pflB gene are~~ is overexpressed in said recombinant microorganism or another nucleotide sequence that codes for the yfiD ORF product ~~and/or the pflB gene product~~ is expressed in said recombinant microorganism;
   b) enriching said L-amino acid in said fermentation medium or in said recombinant microorganism; and
   c) isolating said L-amino acid to produce said L-amino acid product.

2. (Original) The process of claim 1 wherein some or all of the constituents of said fermentation medium and/or the biomass of said recombinant microorganism remain in said L-amino acid product.

3. (Currently amended) The process of claim 1, wherein said recombinant microorganism is made by the transformation of a microorganism of the Enterobacteriaceae family with a vector containing the yfiD ORF ~~and/or the plfB gene~~.

4. (Currently amended) The process of claim 1, wherein the number of copies of ~~said pflB gene and/or~~ said yfiD ORF in said recombinant microorganism is increased by at least 1.

5. (Currently amended) The process of claim 4, wherein the increase in the number of copies of the yfiD ORF ~~and/or of the pflB gene~~ by at least 1 is achieved by integration of said ~~gene or~~ ORF into the chromosome of said recombinant microorganism.

6. (Currently amended) The process of claim 4, wherein the increase in the number of copies of the yfiD ORF ~~and/or of the pflB gene~~ by at least 1 is achieved by means of an extra-chromosomally replicating vector.

7. (Currently amended) The process of claim 1, wherein said overexpression is achieved by:

a) mutating the promoter or the ribosome binding site upstream of said yfiD ORF ~~and/or said pflB gene~~; or

b) incorporating an expression cassette or promoter upstream of said yfiD ORF ~~and/or of said pflB gene~~.

8. (Currently amended) The process of claim 1, wherein said recombinant microorganism is made by the transformation of a microorganism with a polynucleotide coding for the yfiD ORF product ~~and/or a pflB gene product~~ and wherein the expression of said yfiD ORF product ~~and/or a pflB gene product~~ is under the control of a promoter.

9. (Currently amended) The process of claim 1, wherein, through the recombinant engineering of the yfiD ORF ~~and/or pflB gene~~, the concentration or activity of the YfiD gene product ~~and/or of the PflB gene product (protein)~~ is increased by at least 10 %, relative to the activity or concentration of the gene product in the initial strain.

10. (Original) The process of claim 1, wherein the genus of said recombinant microorganism is selected from the group consisting of: Escherichia; Erwinia; Providencia; and Serratia.

11. (Currently amended) The process of claim 1, wherein, said microorganism overexpresses said yfiD ORF ~~and/or said pflB gene~~, and, in addition, at least one gene in the biosynthesis pathway of said L-amino acid is also overexpressed.

12. (Currently amended) The process of claim 1, wherein said microorganism ~~overexpressed~~ overexpresses aid yfiD ORF ~~and/or said pflB gene~~, and, in addition, the activity of one or more additional genes is enhanced, said one or more additional genes being selected from the group consisting of:

a) the thrABC operon coding for aspartate kinase, homoserine dehydrogenase, homoserine kinase and threonine synthase;

b) the pyc gene coding for pyruvate carboxylase;

c) the pps gene for phosphoenolpyruvate synthase;

d) the ppc gene coding for phosphoenolpyruvate carboxylase;

e) the genes pntA and pntB coding for transhydrogenase;

f) the rhtB gene imparting homoserine resistance;

g) the mqo gene coding for malate:quinone oxidoreductase;

h) the rhtC gene imparting threonine resistance;

i) the thrE gene coding for the threonine-export protein;

j) the gdhA gene coding for glutamate dehydrogenase;

k) the hns gene coding for the DNA binding protein HLP-II;

l) the pgm gene coding for phosphoglucomutase;

m) the fba gene coding for fructose biphosphate aldolase;

n) the ptsH gene coding for phosphohistidine protein hexose phosphotransferase;

o) the ptsI gene coding for enzyme I of the phosphotransferase system;

p) the crr gene coding for the glucose-specific IIA component;

q) the ptsG gene coding for the glucose-specific IIBC component;

r) the lrp gene coding for the regulator of the leucine regulon;

s) the csrA gene coding for the global regulator Csr;

t) the fadR gene coding for the regulator of the fad regulon;

u) the iclR gene coding for the regulator of central intermediary metabolism;

v) the mopB gene coding for the 10 kDa chaperon;

w) the ahpC gene coding for the small subunit of alkyl hydroperoxide reductase;

x) the ahpF gene coding for the large subunit of alkyl hydroperoxide reductase;

y) the cysK gene coding for cysteine synthase A;

z) the cysB gene coding for the regulator of the cys regulon;

aa) the cysJ gene coding for the flavoprotein of NADPH sulfite reductase;

bb) the cysI gene coding for the haemoprotein of NADPH sulfite reductase;

cc) the cysH gene coding for adenylyl sulfate reductase;

dd) the phoB gene coding for the positive regulator PhoB of the pho regulon;

ee) the phoR gene coding for the sensor protein of the pho regulon;

ff) the phoE gene coding for protein E of the outer cell membrane;

gg) the pykF gene coding for pyruvate kinase I, which is stimulated by fructose;

hh) the pfkB gene coding for 6-phosphofructokinase II;

ii) the malE gene coding for the periplasmic binding protein of maltose transport;

jj) the sodA gene coding for superoxide dismutase;

kk) the rseA gene coding for a membrane protein with anti-sigmaE activity;

ll) the rseC gene coding for a global regulator of the sigmaE factor;

mm) the sucA gene coding for the decarboxylase subunit of 2-ketoglutarate dehydrogenase;

nn) the sucB gene coding for the dihydrolipoyl transsuccinase E2 subunit of 2-ketoglutarate dehydrogenase;

oo) the sucC gene coding for the β-subunit of succinyl-CoA synthetase;

pp) the sucD gene coding for the α-subunit of succinyl-CoA synthetase;

qq) the adk gene coding for adenylate kinase;

rr) the hdeA gene coding for a periplasmic protein with chaperonin-type function;

ss) the hdeB gene coding for a periplasmic protein with chaperonin-type function;

tt) the icd gene coding for isocitrate dehydrogenase;

uu) the mglB gene coding for the periplasmic, galactose-binding transport protein;

vv) the lpd gene coding for dihydrolipoamide dehydrogenase;

ww) the aceE gene coding for the E1 component of the pyruvate-dehydrogenase complex;

xx) the aceF gene coding for the E2 component of the pyruvate-dehydrogenase complex;

yy) the pepB gene coding for aminopeptidase B;

zz) the aldH gene coding for aldehyde dehydrogenase,

aaa) the bfr gene coding for the iron-storage homoprotein;

bbb) the udp gene coding for uridine phosphorylase; and

ccc) the rseB gene coding for the regulator of sigmaE-factor activity.

13.-14. Cancelled.

15. (Currently amended) The process of any one of claims ~~1-14~~ 1-12, wherein said L-amino acid is selected from the group consisting of: L-asparagine, L-serine, L-glutamate, L-glycine, L-alanine, L-cysteine, L-valine, L-methionine, L-isoleucine, L-leucine, L-tyrosine, L-phenylalanine, L-histidine, L-lysine, L-tryptophan and L-arginine.

16. (Currently amended) The process of any one of claims ~~1-14~~ 1-12, wherein said L-amino acid is selected from the group consisting of: L-isoleucine, L-valine, L-methionine, L-homoserine and L-lysine are produced.

17. (Currently amended) The process of any one of claims ~~1-14~~ 1-12, wherein said L-amino acid is L-threonine.

18.-20. Cancelled.